

STIC Biotechnology Systems Branch
RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/797,553D
Source: IFWO
Date Processed by STIC: 1/31/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/799,8530

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa
"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING DATE: 01/31/2006
 PATENT APPLICATION: US/10/797,553D TIME: 15:21:14

Input Set : A:\1092 US PCT SEQ LIST.1.25.06.txt
 Output Set: N:\CRF4\01312006\J797553D.raw

3 <110> APPLICANT: Moyle, William R.
 4 Xing, Yongna
 6 <120> TITLE OF INVENTION: Protein Knobs
 8 <130> FILE REFERENCE: 1092/US PCT
 10 <140> CURRENT APPLICATION NUMBER: 10/797,553D
 11 <141> CURRENT FILING DATE: 2004-03-10
 13 <160> NUMBER OF SEQ ID NOS: 66
 15 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

2123 <210> SEQ ID NO: 56
 2124 <211> LENGTH: 36 37 shown below
 2125 <212> TYPE: PRT
 2126 <213> ORGANISM: Artificial Sequence
 2128 <220> FEATURE: 2227 This needs explanation
 2129 <223> OTHER INFORMATION: Xaa is any amino acid in the tail portion and some of the
 Xaa 2130 may be missing from the tail portion Please list Xaa locations
 2132 <400> SEQUENCE: 56 on 2227 line. Add 2227 line
 W--> 2134 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Asp Asp Lys Ser
 E--> 2135 1 5 10 15 15 G mesolegied
 2138 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
 E--> 2139 20 20 25 25 30 30 amino acid
 2142 Xaa Xaa Xaa Xaa Xaa number
 E--> 2143 . . 35 35
 (see item 3 on
 Error Summary
 Sheet)

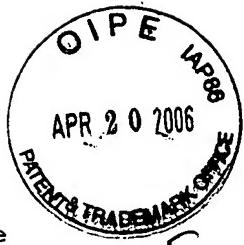
10/19/88, 55302



<210> 2
<211> 92
<212> PRT
<213> Artificial Sequence
<220> *what is its source?*
<223> hCG alpha-subunit with Cys substituted for Gln5

Please correct this
in subsequent
sequences, too!

10/99,55303



<210> 28
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> hCG alpha-subunit with Cys substituted for Ser64
<400> 28

Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro
1 5 10 15

Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys
20 25 30

Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu
35 40 45

Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Cys Ser
50 55 60

Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr
65 70 75 80

Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
85 90

Ser is at location 64

4

VERIFICATION SUMMARY DATE: 01/31/2006
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Input Set : A:\1092 US PCT SEQ LIST.1.25.06.txt
Output Set: N:\CRF4\01312006\J797553D.raw

L:2134 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:56
L:2134 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:56
L:2134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:2135 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:56
M:341 Repeated in SeqNo=56
M:332 Repeated in SeqNo=56
L:2143 M:252 E: No. of Seq. differs, <211> LENGTH:Input:36 Found:37 SEQ:56